

SEQUENCE LISTING

<110> McDonald, John R.
Coggins, Philip

<120> METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
OTHER INFLAMMATORY CONDITIONS AND DISORDERS

<130> 25020-601B

<140> Unassigned

<141> 1999-07-22

<160> 70

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 1

Gly Gly Gly Gly Ser
1 5

<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> REPEAT

<222> (1)...(5)

<223> homo sapien

<400> 2

Gly Gly Gly Gly Ser
1 5

<210> 3

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 3

Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
1 5 10

<210> 4

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien

<400> 4

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 5
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 5
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr
1 5 10 15
Lys Gly

<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 6
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 7
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 7
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15
Lys Gly

<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 8
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe
1 5 10

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> homo sapien

<400> 9
Ser Arg Ser Ser Gly
1 5

<210> 10
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Sequence

<400> 10

Ser Gly Ser Ser Cys
1 5

<210> 11

<211> 28

<212> PRT

<213> diphtheria toxin trypsin sensitive linker

<400> 11

Ala Met Gly Arg Ser Gly Gly Gly Cys Ala Gly Asn Arg Val Gly Ser
1 5 10 15
Ser Leu Ser Cys Gly Gly Leu Asn Leu Gln Ala Met
20 25

<210> 12

<211> 6

<212> PRT

<213> homo sapien

<220>

<221> REPEAT

<222> (3)...(3)

<223> repeat unit 2-4 times

<221> REPEAT

<222> (3)...(4)

<223> repeat family 1-11 times

<400> 12

Ala Met Gly Ser Ala Met
1 5

<210> 13

<211> 74

<212> PRT

<213> homo sapien

<400> 13

Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn Arg
1 5 10 15
Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser Gly
20 25 30
Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys Asp
35 40 45
Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys Tyr
50 55 60
Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
65 70

<210> 14

<211> 77

<212> PRT

<213> homo sapien

<400> 14

Gly Pro Val Ser Ala Val Leu Thr Glu Leu Arg Cys Thr Cys Leu Arg
1 5 10 15
Val Thr Leu Arg Val Asn Pro Lys Thr Ile Gly Lys Leu Gln Val Phe
20 25 30
Pro Ala Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys
35 40 45

Asn Gly Lys Gln Val Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys
 50 55 60
 Val Ile Gln Lys Ile Leu Asp Ser Gly Asn Lys Lys Asn
 65 70 75

<210> 15
 <211> 127
 <212> PRT
 <213> homo sapien

<400> 15
 Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val
 1 5 10 15
 Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr
 20 25 30
 Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp
 35 40 45
 Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln
 50 55 60
 Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met
 65 70 75 80
 Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys
 85 90 95
 Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp
 100 105 110
 Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 115 120 125

<210> 16
 <211> 73
 <212> PRT
 <213> homo sapien

<400> 16
 Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln
 1 5 10 15
 Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly
 20 25 30
 Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg
 35 40 45
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile Ile Glu
 50 55 60
 Lys Met Leu Asn Ser Asp Lys Ser Asn
 65 70

<210> 17
 <211> 73
 <212> PRT
 <213> homo sapien

<400> 17
 Lys Ser Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu
 1 5 10 15
 Gln Glu Ile Pro Leu Arg Ala Ile Leu Cys Tyr Arg Asn Thr Ser Ser
 20 25 30
 Ile Cys Ser Asn Glu Gly Leu Ile Phe Lys Leu Lys Arg Gly Lys Glu
 35 40 45
 Ala Cys Ala Leu Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met
 50 55 60
 Leu Arg His Cys Pro Ser Lys Arg Lys
 65 70

<210> 18
 <211> 133
 <212> PRT

<213> homo sapien

<400> 18
Ala Pro Met Thr Gln Thr Thr Pro Leu Lys Thr Ser Trp Val Asn Cys
1 5 10 15
Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu
20 25 30
Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu
35 40 45
Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala
50 55 60
Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys Asn
65 70 75 80
Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His Pro
85 90 95
Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu Thr
100 105 110
Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr Leu
115 120 125
Ser Leu Ala Ile Phe
130

<210> 19

<211> 77

<212> PRT

<213> homo sapien

<400> 19
Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys
1 5 10 15
Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg Val
20 25 30
Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys Leu
35 40 45
Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln
50 55 60
Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
65 70 75

<210> 20

<211> 76

<212> PRT

<213> homo sapien

<400> 20
Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Thr
1 5 10 15
Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Thr
20 25 30
Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Ala
35 40 45
Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Met
50 55 60
Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr
65 70 75

<210> 21

<211> 76

<212> PRT

<213> homo sapien

<400> 21
Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15
Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30
Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly

35 40 45
 Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
 50 55 60
 Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
 65 70 75

<210> 22
 <211> 76
 <212> PRT
 <213> homo sapien

<400> 22
 Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile
 1 5 10 15
 Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr
 20 25 30
 Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp
 35 40 45
 Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met
 50 55 60
 Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
 65 70 75

<210> 23
 <211> 75
 <212> PRT
 <213> homo sapien

<400> 23
 Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
 1 5 10 15
 Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
 20 25 30
 Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
 35 40 45
 Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
 50 55 60
 His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
 65 70 75

<210> 24
 <211> 70
 <212> PRT
 <213> homo sapien

<400> 24
 Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr
 1 5 10 15
 Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser
 20 25 30
 Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg
 35 40 45
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser
 50 55 60
 Asp Leu Glu Leu Ser Ala
 65 70

<210> 25
 <211> 129
 <212> PRT
 <213> homo sapien

<400> 25
 His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser
 1 5 10 15
 Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile

<210> 29
 <211> 68
 <212> PRT
 <213> homo sapien

<400> 29
 Ser Pro Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala
 1 5 10 15
 Arg Pro Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly
 20 25 30
 Lys Cys Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln
 35 40 45
 Val Cys Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser
 50 55 60
 Leu Glu Met Ser
 65

<210> 30
 <211> 69
 <212> PRT
 <213> homo sapien

<400> 30
 Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys Phe Ser Tyr Thr
 1 5 10 15
 Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr Tyr Glu Thr Ser
 20 25 30
 Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr Lys Arg Ser Lys
 35 40 45
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln Glu Tyr Val Tyr
 50 55 60
 Asp Leu Glu Leu Asn
 65

<210> 31
 <211> 323
 <212> PRT
 <213> homo sapien

<400> 31
 Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser
 1 5 10 15
 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala
 20 25 30
 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp
 35 40 45
 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu
 50 55 60
 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn
 65 70 75 80
 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala
 85 90 95
 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu
 100 105 110
 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly
 115 120 125
 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His
 130 135 140
 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser
 145 150 155 160
 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser
 165 170 175
 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu
 180 185 190
 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Val Ser
 195 200 205

His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile
 210 215 220
 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu
 225 230 235 240
 Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
 245 250 255
 His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
 260 265 270
 His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
 275 280 285
 Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
 290 295 300
 Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
 305 310 315 320
 Asn Glu Leu

<210> 32
 <211> 74
 <212> PRT
 <213> homo sapien

<400> 32
 Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe
 1 5 10 15
 Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn
 20 25 30
 Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn
 35 40 45
 Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu
 50 55 60
 Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
 65 70

<210> 33
 <211> 71
 <212> PRT
 <213> homo sapien

<400> 33
 Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys Leu Glu Tyr Phe Lys
 1 5 10 15
 Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp Tyr Gln Thr Ser Glu
 20 25 30
 Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr Val Gln Gly Arg Ala
 35 40 45
 Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys Asn Ala Val Lys Tyr
 50 55 60
 Leu Gln Ser Leu Glu Arg Ser
 65 70

<210> 34
 <211> 247
 <212> PRT
 <213> Bryonia dioica

<400> 34
 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val
 1 5 10 15
 Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val Tyr
 20 25 30
 Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Ser Gly Arg Tyr Thr
 35 40 45
 Leu Leu His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Val
 50 55 60
 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val Ser
 65 70 75 80

Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Phe Val Phe
 85 90 95
 Lys Asp Ala Lys Lys Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
 100 105 110
 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
 115 120 125
 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Tyr Tyr Thr Ala
 130 135 140
 Ser Ser Ala Ala Ser Ala Leu Val Leu Ile Gln Ser Thr Ala Glu
 145 150 155 160
 Ser Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
 165 170 175
 Lys Thr Phe Leu Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Asn Trp
 180 185 190
 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
 195 200 205
 Phe Glu Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val Ser
 210 215 220
 Ile Thr Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu Leu
 225 230 235 240
 Leu Asn Arg Asn Asn Ile Ala
 245

<210> 35
 <211> 275
 <212> PRT
 <213> Saponaria officinalis

<400> 35
 Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr
 1 5 10 15
 Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu
 20 25 30
 Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu
 35 40 45
 Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu
 50 55 60
 Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp
 65 70 75 80
 Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser
 85 90 95
 Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys
 100 105 110
 Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln
 115 120 125
 Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp
 130 135 140
 Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val
 145 150 155 160
 Lys Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu
 165 170 175
 Ala Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro
 180 185 190
 Asn Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp
 195 200 205
 Lys Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe
 210 215 220
 Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp
 225 230 235 240
 Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ser Ser Asn
 245 250 255
 Glu Ala Asn Ser Thr Val Arg His Tyr Gly Pro Leu Lys Pro Thr Leu
 260 265 270
 Leu Ile Thr
 275

<210> 36

<211> 250
 <212> PRT
 <213> Momordica charantia

<400> 36
 Ala Pro Thr Leu Glu Thr Ile Ala Ser Leu Asp Leu Asn Asn Pro Thr
 1 5 10 15
 Thr Tyr Leu Ser Phe Ile Thr Asn Ile Arg Thr Lys Val Ala Asp Lys
 20 25 30
 Thr Glu Gln Cys Thr Ile Gln Lys Ile Ser Lys Thr Phe Thr Gln Arg
 35 40 45
 Tyr Ser Tyr Ile Asp Leu Ile Val Ser Ser Thr Gln Lys Ile Thr Leu
 50 55 60
 Ala Ile Asp Met Ala Asp Leu Tyr Val Leu Gly Tyr Ser Asp Ile Ala
 65 70 75 80
 Asn Asn Lys Gly Arg Ala Phe Phe Phe Lys Asp Val Thr Glu Ala Val
 85 90 95
 Ala Asn Asn Phe Phe Pro Gly Ala Thr Gly Thr Asn Arg Ile Lys Leu
 100 105 110
 Thr Phe Thr Gly Ser Tyr Gly Asp Leu Glu Lys Asn Gly Gly Leu Arg
 115 120 125
 Lys Asp Asn Pro Leu Gly Ile Phe Arg Leu Glu Asn Ser Ile Val Asn
 130 135 140
 Ile Tyr Gly Lys Ala Gly Asp Val Lys Lys Gln Ala Lys Phe Phe Leu
 145 150 155 160
 Leu Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Ser
 165 170 175
 Asp Lys Ile Pro Ser Glu Lys Tyr Glu Glu Val Thr Val Asp Glu Tyr
 180 185 190
 Met Thr Ala Leu Glu Asn Asn Trp Ala Lys Leu Ser Thr Ala Val Tyr
 195 200 205
 Asn Ser Lys Pro Ser Thr Thr Thr Ala Thr Lys Cys Gln Leu Ala Thr
 210 215 220
 Ser Pro Val Thr Ile Ser Pro Trp Ile Phe Lys Thr Val Glu Glu Ile
 225 230 235 240
 Lys Leu Val Met Gly Leu Leu Lys Ser Ser
 245 250

<210> 37
 <211> 293
 <212> PRT
 <213> Shigella dysenteriae

<400> 37
 Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser
 1 5 10 15
 Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser
 20 25 30
 Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn
 35 40 45
 Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe
 50 55 60
 Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly
 65 70 75 80
 Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser
 85 90 95
 His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser
 100 105 110
 Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met
 115 120 125
 Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser
 130 135 140
 His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg
 145 150 155 160
 Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg
 165 170 175
 Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met

180 185 190
 Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser
 195 200 205
 Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile
 210 215 220
 Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu
 225 230 235
 Asn Cys His His His Ala Ser Arg Val Ala Arg Met Ala Ser Asp Glu
 245 250 255
 Phe Pro Ser Met Cys Pro Ala Asp Gly Arg Val Arg Gly Ile Thr His
 260 265 270
 Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu Gly Ala Ile Leu Met Arg
 275 280 285
 Arg Thr Ile Ser Ser
 290

<210> 38
 <211> 319
 <212> PRT
 <213> Escherichia coli

<400> 38
 Met Lys Cys Ile Leu Phe Lys Trp Val Leu Cys Leu Leu Leu Gly Phe
 1 5 10 15
 Ser Ser Val Ser Tyr Ser Arg Glu Phe Thr Ile Asp Phe Ser Thr Gln
 20 25 30
 Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Glu Ile Ser Thr
 35 40 45
 Pro Leu Glu His Ile Ser Gln Gly Thr Thr Ser Val Ser Val Ile Asn
 50 55 60
 His Thr Pro Pro Gly Ser Tyr Phe Ala Val Asp Ile Arg Gly Leu Asp
 65 70 75 80
 Val Tyr Gln Ala Arg Phe Asp His Leu Arg Leu Ile Ile Glu Gln Asn
 85 90 95
 Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Ala Thr Asn Thr Phe Tyr
 100 105 110
 Arg Phe Ser Asp Phe Thr His Ile Ser Val Pro Gly Val Thr Thr Val
 115 120 125
 Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Ala
 130 135 140
 Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser Ser
 145 150 155 160
 Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp Ala
 165 170 175
 Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg
 180 185 190
 Phe Arg Gln Ile Gln Arg Glu Phe Arg Gln Ala Leu Ser Glu Thr Ala
 195 200 205
 Pro Val Tyr Thr Met Thr Pro Gly Asp Val Asp Leu Thr Leu Asn Trp
 210 215 220
 Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Asp Gly Val
 225 230 235 240
 Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly Thr
 245 250 255
 Val Ala Val Ile Leu Asn Cys His His Gln Gly Ala Arg Ser Val Arg
 260 265 270
 Ala Val Asn Glu Glu Ser Gln Pro Glu Cys Gln Ile Thr Gly Asp Arg
 275 280 285
 Pro Val Ile Lys Ile Asn Asn Thr Leu Trp Glu Ser Asn Thr Ala Ala
 290 295 300
 Ala Phe Leu Asn Arg Lys Ser Gln Phe Leu Tyr Thr Thr Gly Lys
 305 310 315

<210> 39
 <211> 247
 <212> PRT
 <213> Trichosanthews kirilowii

<400> 39
 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Ser Ser Ser Tyr Gly Val
 1 5 10 15
 Phe Ile Ser Asn Leu Arg Lys Ala Leu Pro Asn Glu Arg Lys Leu Tyr
 20 25 30
 Asp Ile Pro Leu Leu Arg Ser Ser Leu Pro Gly Ser Gln Arg Tyr Ala
 35 40 45
 Leu Ile His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Ile
 50 55 60
 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Arg Ala Gly Asp Thr Ser
 65 70 75 80
 Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Tyr Val Phe
 85 90 95
 Lys Asp Ala Met Arg Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
 100 105 110
 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
 115 120 125
 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Phe Tyr Tyr Asn Ala
 130 135 140
 Asn Ser Ala Ala Ser Ala Leu Met Val Leu Ile Gln Ser Thr Ser Glu
 145 150 155 160
 Ala Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
 165 170 175
 Lys Thr Phe Leu Pro Ser Leu Ala Ile Ile Ser Leu Glu Asn Ser Trp
 180 185 190
 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln
 195 200 205
 Phe Glu Ser Pro Val Val Leu Ile Asn Ala Gln Asn Gln Arg Val Thr
 210 215 220
 Ile Thr Asn Val Asp Ala Gly Val Val Thr Ser Asn Ile Ala Leu Leu
 225 230 235 240
 Leu Asn Arg Asn Asn Met Ala
 245

<210> 40
 <211> 88
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapien His-Tag leader sequence

<400> 40

aaggagatatacc atg ggc agc agc cat cat cat cat cac agc agc
 Met Gly Ser Ser His His His His His Ser Ser
 1 5 10

43

ggc ctg gtg ccg cgc ggc agc cat atg ctc gag gat ccg
 Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro
 15 20 25

82

<210> 41
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Homo sapien forward primer (Eotaxin)

<400> 41

gggtaatagc atatggggcc agcttctgtc ccaacca

37

<210> 42
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (Eotaxin)

<400> 42

cccgaattct ttcacgcgtg gctttggagt tggagatttt tggt

44

<210> 43
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien forward primer (MCP-1)

<400> 43
gggtaatagc atatgcagcc agatgcaatc aatgcccga

39

<210> 44
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (MCP-1)

<400> 44

cccgaattct ttcacgcag tcttcggagt ttgggtttct t

41

<210> 45
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien forward primer (MCP-3)

<400> 45
catatgcaac cggtaggcac caacacg

27

<210> 46
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo sapien reverse primer (MCP-3)

<400> 46
cactagtaac catcgcaagc ttcggggtct gag

33

<210> 47
<211> 38

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Homo sapien forward primer (SDF-1■)

 <400> 47
 gggtaatagc atatgaagcc cgtcagcctg agctacag 38

 <210> 48
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Homo sapien reverse primer (SDF-1■)

 <400> 48
 cccgaattct ttcacgcca tcttgaacct cttgtttaaa gctttc 46

 <210> 49
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Shigella dysenteriae forward primer (Shiga)

 <400> 49
 gggtaatagc atatgaaaga attcaccctg gacttttcc 39

 <210> 50
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Shigella dysenteriae reverse primer (Shiga)

 <400> 50
 cccggatcca ctagtattaa gcgtgggtg 28

 <210> 51
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Shigella dysenteriae reverse primer (Shiga-His6)

 <400> 51
 cccggatcca ctagtttaat gatgatggtg gtggtggcaa ttgag 45

 <210> 52
 <211> 978
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> CDS
 <222> (1) .. (978)

 <220>

<223> Description of Artificial Sequence: Construct encoding chemokine-fusion protein MCP1-AM-truncated Shiga-A1 Subunit toxin

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<400> 52
atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
1 5 10 15

acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
20 25 30

acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
35 40 45

gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
50 55 60

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg aaa 240
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys
65 70 75 80

gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg 288
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu
85 90 95

aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc 336
Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser
100 105 110

ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg 384
Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu
115 120 125

ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat 432
Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn
130 135 140

aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt 480
Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe
145 150 155 160

gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac 528
Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His
165 170 175

gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct 576
Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser
180 185 190

tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa 624
Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln
195 200 205

atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat 672
Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His
210 215 220

tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc 720
Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe
225 230 235 240

gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc 768

```


Leu Arg Phe Arg Gln Ile Gln Arg Gly
 250 255
 ctg tct ggc cgc agc tat gtg atg act 816
 Leu Ser Gly Arg Ser Tyr Val Met Thr
 265 270
 ctg aac tgg ggt cgc ttg tct tcc gtt 864
 Leu Asn Trp Gly Arg Leu Ser Ser Val
 280 285
 gat tct gtc cgt gtt ggc cgt atc agc 912
 Asp Ser Val Arg Val Gly Arg Ile Ser
 300
 cta ggc tcc gtc gca ctg att ctc aat 960
 Leu Gly Ser Val Ala Leu Ile Leu Asn
 315 320
 978

cial Sequence: Construct encoding chemokine-
 -truncated Shiga-A1 Subunit HIS6

gcc cca gtc acc tgc tgt tat aac ttc 48
 Ala Pro Val Thr Cys Cys Tyr Asn Phe
 10 15
 cag agg ctc gcg agc tat aga aga atc 96
 Gln Arg Leu Ala Ser Tyr Arg Arg Ile
 25 30
 gaa gct gtg atc ttc aag acc att gtg 144
 Glu Ala Val Ile Phe Lys Thr Ile Val
 40 45
 ccc aag cag aag tgg gtt cag gat tcc 192
 Pro Lys Gln Lys Trp Val Gln Asp Ser
 5 60
 a acc caa act ccg aag act gcg atg aaa 240
 n Thr Gln Thr Pro Lys Thr Ala Met Lys
 75 80
 c act gca aaa act tac gtc gat agc ctg 288
 r Thr Ala Lys Thr Tyr Val Asp Ser Leu
 90 95
 c ggt acg ccg ctg caa acg att tcc agc 336
 e Gly Thr Pro Leu Gln Thr Ile Ser Ser

100	105	110	
ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu 115 120 125			384
ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn 130 135 140			432
aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe 145 150 155 160			480
gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His 165 170 175			528
gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser 180 185 190			576
tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln 195 200 205			624
atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His 210 215 220			672
tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe 225 230 235 240			720
gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly 245 250 255			768
ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr 260 265 270			816
gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val 275 280 285			864
ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser 290 295 300			912
ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn 305 310 315 320			960
tgc cac cac cac cat cat cat taa Cys His His His His His His 325			984

<210> 54
 <211> 999
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(999)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP1-AM-SAPORIN

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<400> 54
atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
1 5 10 15

acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
20 25 30

acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
35 40 45

gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
50 55 60

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg gtt 240
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Val
65 70 75 80

act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc 288
Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser
85 90 95

agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa 336
Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys
100 105 110

tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag 384
Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys
115 120 125

ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc 432
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly
130 135 140

ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat 480
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn
145 150 155 160

acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg 528
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala
165 170 175

gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca 576
Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala
180 185 190

ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc 624
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile
195 200 205

acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg 672
Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu
210 215 220

ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa 720
Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys
225 230 235

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gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc 768
 Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala 255
 245
 gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac 816
 Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn 270
 260
 aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa 864
 Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys 285
 275
 aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat 912
 Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn 300
 290
 aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg 960
 Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 320
 305
 caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa 999
 Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys 330
 325
 325 330

<210> 55
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 Subunit

<400> 55
 atg caa ccg gta ggc atc aac acg tcg acc acg tgc tgt tat cgc ttt 48
 Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe 15
 1 5 10
 atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc 96
 Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr 30
 20 25
 act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctc 144
 Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu 45
 35 40
 gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt 192
 Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe 60
 50 55
 atg aaa cat ctg gat aag aaa act cag acc ccg aag ctt gcg atg aaa 240
 Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu Ala Met Lys 80
 65 70 75
 gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg 288
 Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu 95
 85 90

aat	gtg	att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	tcc	agc	336
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	
			100					105					110			
ggg	ggg	act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	aac	ttg	384
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	
		115					120					125				
ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	432
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	
	130					135					140					
aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggg	ttt	480
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	
145					150					155					160	
gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	528
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	
				165					170					175		
gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	576
Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	
			180					185					190			
tat	act	acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	atg	caa	624
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	
		195					200					205				
atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	672
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	
	210					215					220					
tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	ggc	atg	ctg	cgc	ttc	720
Ser	Gly	Thr	Ser	Leu	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe		
225				230					235					240		
gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	768
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	
				245					250					255		
ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	816
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	
			260					265					270			
gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	tcc	gtt	864
Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	
		275					280					285				
ctg	ccg	gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	912
Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	
		290				295					300					
ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	960
Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	
305					310					315					320	
tgc	cac	cac	cac	gct	taa											978
Cys	His	His	His	Ala												
				325												

<210> 56
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1)..(984)

<220>

<223> Description of Artificial Sequence: ce: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 subunit HIS6

<400> 56

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Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	
1				5					10					15		
atc	aac	aag	aaa	atc	ccg	aaa	caa	cgc	ctg	gaa	tcc	tat	cgt	cgc	acc	96
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	
			20					25					30			
act	agc	agc	cac	tgt	ccg	cgc	gaa	gca	gtc	atc	ttc	aaa	acc	aag	ctc	144
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	
			35				40					45				
gat	aag	gaa	atc	tgt	gca	gac	ccg	act	cag	aaa	tgg	gtg	caa	gat	ttt	192
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	
	50					55					60					
atg	aaa	cat	ctg	gat	aag	aaa	act	cag	acc	ccg	aag	ctt	gcg	atg	aaa	240
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu	Ala	Met	Lys	
	65				70					75					80	
gaa	ttc	acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	agc	ctg	288
Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	
				85					90					95		
aat	gtg	att	cgt	tcc	gcg	atc	ggc	acg	ccg	ctg	caa	acg	att	tcc	agc	336
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	
			100				105						110			
ggc	ggc	act	tcc	ctc	ctg	atg	att	gat	tcc	ggc	acg	ggc	gat	aac	ttg	384
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	
		115				120						125				
ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	432
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	
	130					135					140					
aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggc	ttt	480
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	
	145				150					155					160	
gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	528
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	
				165					170					175		
gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	576
Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	
			180					185					190			
tat	act	acg	tta	cag	cgt	gtg	gct	ggc	atc	agc	cgc	act	ggc	atg	caa	624
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	
		195				200						205				
atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	672
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	
	210					215					220					
tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	720
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	
	225				230					235					240	

gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc	768
Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly	
245 250 255	
ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act	816
Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr	
260 265 270	
gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt	864
Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val	
275 280 285	
ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc	912
Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser	
290 295 300	
ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat	960
Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn	
305 310 315 320	
tgc cac cac cac cat cat cat taa	984
Cys His His His His His His	
325	

<210> 57
 <211> 999
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(999)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin Fusion Protein MCP3-AM-SAPORIN

<400> 57

atg caa ccg gta ggc atc aac acg tcc acc acg tgc tgt tat cgc ttt	48
Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe	
1 5 10 15	
atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc	96
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr	
20 25 30	
act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctc	144
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu	
35 40 45	
gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt	192
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe	
50 55 60	
atg aaa cat ctg gat aag aaa act cag acc ccg aag ctt gcg atg gtt	240
Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu Ala Met Val	
65 70 75 80	
act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc	288
Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser	
85 90 95	
agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa	336
Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys	

100	105	110	
tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys 115 120 125			384
ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly 130 135 140			432
ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn 145 150 155 160			480
acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala 165 170 175			528
gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala 180 185 190			576
ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile 195 200 205			624
acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu 210 215 220			672
ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys 225 230 235 240			720
gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala 245 250 255			768
gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn 260 265 270			816
aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys 275 280 285			864
aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn 290 295 300			912
aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 305 310 315 320			960
caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys 325 330			999

<210> 58

<211> 963

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-truncated Shiga-A1 Subunit

<220>
 <221> CDS
 <222> (1) .. (963)

<400> 58
 aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc 48
 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1 5 10 15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca 96
 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
 20 25 30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa 144
 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
 35 40 45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa 192
 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 50 55 60

gct tta aac aag agg ttc aag atg gcg atg aaa gaa ttc acc ctg gac 240
 Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp
 65 70 75 80

ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg att cgt tcc 288
 Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser
 85 90 95

gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt act tcc ctc 336
 Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu
 100 105 110

ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct gtt gat gtg 384
 Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val
 115 120 125

cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg cgt ctg atc 432
 Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile
 130 135 140

gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac cgt acg aac 480
 Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn
 145 150 155 160

aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg ttt ccg ggc 528
 Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly
 165 170 175

acc act gct gtt act ctg agc ggc gat tct tct tat act acg tta cag 576
 Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln
 180 185 190

cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat cgc cat tct 624
 Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser
 195 200 205

ctg acg acc agc tat ctg gac tta atg agc cat tct ggc acc agc ctg 672
 Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu
 210 215 220

acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg gtc acc gcc 720
 Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala
 225 230 235 240

gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc acc act tta	768
Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu	
245 250 255	
gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa gat gtc gat	816
Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp	
260 265 270	
ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg gat tat cac	864
Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His	
275 280 285	
ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc tct att aat	912
Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn	
290 295 300	
gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac cac cac gct	960
Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His His His Ala	
305 310 315 320	
taa	963

<210> 59

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-truncated Shiga-A1 Subunit HIS6

<220>

<221> CDS

<222> (1)..(969)

<400> 59

aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc	48
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser	
1 5 10 15	
cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca	96
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro	
20 25 30	
aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa	144
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln	
35 40 45	
gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa	192
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys	
50 55 60	
gct tta aac aag agg ttc aag atg gcg atg aaa gaa ttc acc ctg gac	240
Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp	
65 70 75 80	
ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg att cgt tcc	288
Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser	
85 90 95	
gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt act tcc ctc	336
Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu	
100 105 110	

ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct gtt gat gtg	384
Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val	
115 120 125	
cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg cgt ctg atc	432
Arg Gly Ile Asp Pro Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile	
130 135 140	
gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac cgt acg aac	480
Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn	
145 150 155 160	
aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg ttt ccg ggc	528
Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly	
165 170 175	
acc act gct gtt act ctg agc ggc gat tct tct tat act acg tta cag	576
Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Leu Gln	
180 185 190	
cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat cgc cat tct	624
Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser	
195 200 205	
ctg acg acc agc tat ctg gac tta atg agc cat tct ggc acc agc ctg	672
Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu	
210 215 220	
acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg gtc acc gcc	720
Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala	
225 230 235 240	
gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc acc act tta	768
Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu	
245 250 255	
gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa gat gtc gat	816
Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp	
260 265 270	
ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg gat tat cac	864
Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His	
275 280 285	
ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc tct att aat	912
Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn	
290 295 300	
gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac cac cac cat	960
Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His His His His	
305 310 315 320	
cat cat taa	969
His His	

<210> 60

<211> 984

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF1-AM-SAPORIN

<220>
 <221> CDS
 <222> (1) .. (984)

<400> 60
 aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc 48
 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1 5 10 15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca 96
 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
 20 25 30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa 144
 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
 35 40 45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa 192
 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 50 55 60

gct tta aac aag agg ttc aag atg gcg atg gtt act agt att acc ctg 240
 Ala Leu Asn Lys Arg Phe Lys Met Ala Met Val Thr Ser Ile Thr Leu
 65 70 75 80

gac ctg gtc aat ccg acc gcc ggc caa tat agc agc ttc gtg gat aag 288
 Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys
 85 90 95

att cgt aac aac gta aaa gat ccg aat ctg aaa tac ggt ggt act gat 336
 Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp
 100 105 110

att gcg gtc atc ggt ccg ccg agc aaa gaa aag ttc ctg cgc att aac 384
 Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn
 115 120 125

ttt caa agc tcc cgt ggc act gtt tct ctg ggc ctg aag cgc gat aac 432
 Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn
 130 135 140

ctg tat gtt gtt gcc tat ctg gcg atg gat aat acg aac gtg aac cgc 480
 Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg
 145 150 155 160

gcc tac tac ttt cgt agc gag att acg agc gcg gaa tcc act gct ctg 528
 Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser Thr Ala Leu
 165 170 175

ttc ccg gag gcg acc act gca aac caa aaa gca ctg gaa tat acg gaa 576
 Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu
 180 185 190

gat tac cag tcc atc gag aag aac gcg cag atc acc cag ggc gat caa 624
 Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Gln
 195 200 205

tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg ctg agc acg agc atg 672
 Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser Thr Ser Met
 210 215 220

gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa gac gaa gcc cgc ttc 720
 Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu Ala Arg Phe
 225 230 235 240

ctg ctg atc gcc att cag atg acg gca gaa gcc gcc cgt ttc cgc tac 768

Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Ala	Ala	Arg	Phe	Arg	Tyr		
				245					250					255			
att	cag	aac	ctg	gtc	atc	aaa	aac	ttc	ccg	aac	aag	ttc	aat	tcc	gag	816	
Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	Pro	Asn	Lys	Phe	Asn	Ser	Glu		
			260					265					270				
aat	aaa	gtc	att	cag	ttc	gag	ggt	aat	tgg	aaa	aaa	att	tcc	acc	gcc	864	
Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp	Lys	Lys	Ile	Ser	Thr	Ala		
			275				280					285					
att	tat	ggg	gac	gcg	aag	aac	ggg	ggt	ttc	aat	aaa	gat	tat	gat	ttt	912	
Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	Lys	Asp	Tyr	Asp	Phe		
		290				295					300						
ggg	ttc	ggg	aag	gta	cgt	cag	gtg	aaa	gac	ctg	caa	atg	ggg	ctg	ctg	960	
Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	Gln	Met	Gly	Leu	Leu		
					310					315					320		
atg	tac	cta	gga	aaa	ccg	aag	taa									984	
Met	Tyr	Leu	Gly	Lys	Pro	Lys											
				325													

<210> 61
 <211> 972
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(972)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit

<400>	61																
atg	ggg	cca	gct	tct	gtc	cca	acc	acc	tgc	tgc	ttt	aac	ctg	gcc	aat	48	
Met	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	Cys	Phe	Asn	Leu	Ala	Asn		
	1			5					10					15			
agg	aag	ata	ccc	ctt	cag	cga	cta	gag	agc	tac	agg	aga	atc	acc	agt	96	
Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Ile	Thr	Ser		
			20					25					30				
ggc	aaa	tgt	ccc	cag	aaa	gct	gtg	atc	ttc	aag	acc	aaa	ctg	gcc	aag	144	
Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Ala	Lys		
		35				40						45					
gat	atc	tgt	gcc	gac	ccc	aag	aag	aag	tgg	gtg	cag	gat	tcc	atg	aag	192	
Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	Val	Gln	Asp	Ser	Met	Lys		
	50				55				60								
tat	ctg	gac	caa	aaa	tct	cca	act	cca	aag	cca	gcg	atg	aaa	gaa	ttc	240	
Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	Pro	Ala	Met	Lys	Glu	Phe		
	65				70				75					80			
acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	agc	ctg	aat	gtg	288	
Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val		
				85					90					95			
att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	tcc	agc	ggg	ggg	336	
Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly		
			100					105					110				

act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct	384
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala	
115 120 125	
gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg	432
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu	
130 135 140	
cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac	480
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn	
145 150 155 160	
cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg	528
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr	
165 170 175	
ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct tat act	576
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr	
180 185 190	
acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat	624
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn	
195 200 205	
cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat tct ggc	672
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly	
210 215 220	
acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg	720
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr	
225 230 235 240	
gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc	768
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg	
245 250 255	
acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa	816
Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu	
260 265 270	
gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg	864
Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro	
275 280 285	
gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc	912
Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly	
290 295 300	
tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac	960
Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His	
305 310 315 320	
cac cac gct taa	972
His His Ala	

<210> 62
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-

toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit HIS6

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<400> 62
atg ggg cca gct tct gtc cca acc acc tgc tgc ttt aac ctg gcc aat 48
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn
1 5 10 15

agg aag ata ccc ctt cag cga cta gag agc tac agg aga atc acc agt 96
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser
20 25 30

ggc aaa tgt ccc cag aaa gct gtg atc ttc aag acc aaa ctg gcc aag 144
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys
35 40 45

gat atc tgt gcc gac ccc aag aag aag tgg gtg cag gat tcc atg aag 192
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys
50 55 60

tat ctg gac caa aaa tct cca act cca aag cca gcg atg aaa gaa ttc 240
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Lys Glu Phe
65 70 75 80

acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg 288
Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val
85 90 95

att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt 336
Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly
100 105 110

act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct 384
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala
115 120 125

gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg 432
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu
130 135 140

cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac 480
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn
145 150 155 160

cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg 528
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr
165 170 175

ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct tat act 576
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr
180 185 190

acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat 624
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn
195 200 205

cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat tct ggc 672
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly
210 215 220

acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg 720
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr
225 230 235 240

gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc 768
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg

```

245										250										255										
acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	gcc	gaa		816													
Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu															
			260					265					270																	
gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	tcc	gtt	ctg	ccg		864													
Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro															
			275				280					285																		
gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	ttt	ggc		912													
Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly															
			290			295					300																			
tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	tgc	cac		960													
Ser	Ile	Asn	Ala	Ile		Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His															
305					310					315					320															
cac	cac	cat	cat	cat	taa												978													
His	His	His	His	His																										
					325																									

<210> 63
 <211> 993
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(993)

<220>
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-SAPORIN

<400> 63																
atg	ggg	cca	gct	tct	gtc	cca	acc	acc	tgc	tgc	ttt	aac	ctg	gcc	aat	48
Met	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	Cys	Phe	Asn	Leu	Ala	Asn	
1				5					10					15		
agg	aag	ata	ccc	ctt	cag	cga	cta	gag	agc	tac	agg	aga	atc	acc	agt	96
Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	
			20					25					30			
ggc	aaa	tgt	ccc	cag	aaa	gct	gtg	atc	ttc	aag	acc	aaa	ctg	gcc	aag	144
Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Ala	Lys	
		35					40					45				
gat	atc	tgt	gcc	gac	ccc	aag	aag	aag	tgg	gtg	cag	gat	tcc	atg	aag	192
Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	Val	Gln	Asp	Ser	Met	Lys	
		50				55					60					
tat	ctg	gac	caa	aaa	tct	cca	act	cca	aag	cca	gcg	atg	gtt	act	agt	240
Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	Pro	Ala	Met	Val	Thr	Ser	
65					70				75					80		
att	acc	ctg	gac	ctg	gtc	aat	ccg	acc	gcc	ggc	caa	tat	agc	agc	ttc	288
Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	Ser	Phe	
				85					90					95		
gtg	gat	aag	att	cgt	aac	aac	gta	aaa	gat	ccg	aat	ctg	aaa	tac	ggg	336
Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	Tyr	Gly	
			100					105					110			

ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag ttc ctg 384
 Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu
 115 120 125
 cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc ctg aag 432
 Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys
 130 135 140
 cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat acg aac 480
 Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn
 145 150 155 160
 gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg gaa tcc 528
 Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser
 165 170 175
 act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca ctg gaa 576
 Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu
 180 185 190
 tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc acc cag 624
 Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln
 195 200 205
 ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg ctg agc 672
 Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser
 210 215 220
 acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa gac gaa 720
 Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu
 225 230 235 240
 gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc gcc cgt 768
 Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala Ala Arg
 245 250 255
 ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac aag ttc 816
 Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn Lys Phe
 260 265 270
 aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa aaa att 864
 Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys Lys Ile
 275 280 285
 tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat aaa gat 912
 Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp
 290 295 300
 tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg caa atg 960
 Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met
 305 310 315 320
 ggt ctg ctg atg tac cta gga aaa ccg aag taa 993
 Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys
 325 330

<210> 64
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding
 Methionine-truncated Shiga-A1 Subunit fusion protien

<220>

<221> CDS
 <222> (1) .. (744)

<400> 64

atg	aaa	gaa	ttc	acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	48
Met	Lys	Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	
1				5					10					15		
agc	ctg	aat	gtg	att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	96
Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	
			20					25					30			
tcc	agc	ggg	ggg	act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	144
Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	
			35				40					45				
aac	ttg	ttt	gct	ggt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	192
Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	
	50					55					60					
ttt	aat	aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	240
Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	
	65				70					75					80	
ggg	ttt	gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	288
Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	
				85				90						95		
tcc	cac	gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	336
Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	
			100					105					110			
tct	tct	tat	act	acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	384
Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	
		115					120					125				
atg	caa	atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	432
Met	Gln	Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	
	130					135					140					
agc	cat	tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	480
Ser	His	Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	
	145				150				155						160	
cgc	ttc	gtg	acg	gtc	acc	ggc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	528
Arg	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	
				165				170						175		
cgc	ggc	ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	576
Arg	Gly	Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	
			180					185					190			
atg	act	gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	624
Met	Thr	Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	
		195					200					205				
tcc	gtt	ctg	ccg	gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	672
Ser	Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	
		210				215					220					
atc	agc	ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	720
Ile	Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	
	225				230					235					240	
ctc	aat	tgc	cac	cac	cac	gct	taa									744
Leu	Asn	Cys	His	His	His	Ala										
				245												

<210> 65
 <211> 750
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct encoding
 Methionine-truncated Shiga-A1 Subunit HIS6 fusion protein

<220>
 <221> CDS
 <222> (1)..(750)

<400> 65
 atg aaa gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat 48
 Met Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp
 1 5 10 15

agc ctg aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att 96
 Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile
 20 25 30

tcc agc ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat 144
 Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp
 35 40 45

aac ttg ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt 192
 Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg
 50 55 60

ttt aat aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg 240
 Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr
 65 70 75 80

ggt ttt gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc 288
 Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe
 85 90 95

tcc cac gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat 336
 Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp
 100 105 110

tct tct tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt 384
 Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly
 115 120 125

atg caa atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg 432
 Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met
 130 135 140

agc cat tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg 480
 Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu
 145 150 155 160

cgc ttc gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa 528
 Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln
 165 170 175

cgc ggc ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg 576
 Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val
 180 185 190

atg act gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct 624
 Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser
 195 200 205

tcc gtt ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt 672
 Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg
 210 215 220

atc agc ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att 720
 Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile
 225 230 235 240

ctc aat tgc cac cac cac cat cat cat taa 750
 Leu Asn Cys His His His His His His
 245 250

<210> 66

<211> 765

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding
 Methionine-Saporin fusion protein

<220>

<221> CDS

<222> (1)..(765)

<400> 66
 atg gtt act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa 48
 Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln
 1 5 10 15

tat agc agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat 96
 Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn
 20 25 30

ctg aaa tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa 144
 Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys
 35 40 45

gaa aag ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct 192
 Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser
 50 55 60

ctg ggc ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg 240
 Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met
 65 70 75 80

gat aat acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg 288
 Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr
 85 90 95

agc gcg gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa 336
 Ser Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln
 100 105 110

aaa gca ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg 384
 Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala
 115 120 125

cag atc acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att 432
 Gln Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile
 130 135 140

gat ctg ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg 480
 Asp Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val

145	150							155							160			
gtt aaa gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca																		528
Val Lys Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala																		
	165							170							175			
gaa gcc gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc																		576
Glu Ala Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe																		
	180							185							190			
ccg aac aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat																		624
Pro Asn Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn																		
	195							200							205			
tggt aaa aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt																		672
Trp Lys Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val																		
	210							215							220			
ttc aat aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa																		720
Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys																		
	225							230							235			
gac ctg caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa																		765
Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys																		
	245							250							255			

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<210> 67
<211> 231
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (1)..(231)
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<220>
<223> Description of Artificial Sequence: Construct encoding Methionine-MCP2 protein

<400>	67																	48
atg	caa	ccg	gta	ggc	atc	aac	acg	tcg	acc	acg	tgc	tgt	tat	cgc	ttt			
Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe			
1				5					10					15				
																	96	
atc	aac	aag	aaa	atc	ccg	aaa	caa	cgc	ctg	gaa	tcc	tat	cgt	cgc	acc			
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr			
			20					25					30					
																	144	
act	agc	agc	cac	tgt	ccg	cgc	gaa	gca	gtc	atc	ttc	aaa	acc	aag	ctc			
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu			
			35				40					45						
																	192	
gat	aag	gaa	atc	tgt	gca	gac	ccg	act	cag	aaa	tgg	gtg	caa	gat	ttt			
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe			
	50					55					60							
																	231	
atg	aaa	cat	ctg	gat	aag	aaa	act	cag	acc	ccg	aag	ctt						
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu						
65					70					75								

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<210> 68
<211> 4
<212> PRT
<213> Pseudomonas aeruginosa
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<220>
 <223> Pseudomonas toxin carboxy-terminal endoplasmic reticulum retention

signal

<400> 68
 Xaa Asp Glu Leu
 1

<210> 69
 <211> 393
 <212> DNA
 <213> Mus musculus

<220>
 <223> Mouse chemokine ALP cDNA

<220>
 <221> CDS
 <222> (11)..(373)

<400> 69
 ctgagtgc atg atg gag ggg ctc tcc ccc gcc agc agc ctc ccg ctg 49
 Met Met Glu Gly Leu Ser Pro Ala Ser Ser Leu Pro Leu
 1 5 10

tta ctg ttg ctt ctg agc ccg gct cct gaa gca gcc ttg cct ctg ccc 97
 Leu Leu Leu Leu Leu Ser Pro Ala Pro Glu Ala Ala Leu Pro Leu Pro
 15 20 25

tcc agc act agc tgc tgt act cag ctc tat aga cag cca ctc cca agc 145
 Ser Ser Thr Ser Cys Cys Thr Gln Leu Tyr Arg Gln Pro Leu Pro Ser
 30 35 40 45

agg ctg ctg agg agg att gtc cac atg gaa ctg cag gag gcc gat ggg 193
 Arg Leu Leu Arg Arg Ile Val His Met Glu Leu Gln Glu Ala Asp Gly
 50 55 60

gac tgt cac ctc cag gct gtc gtg ctt cac ctg gct cgg cgc agt gtc 241
 Asp Cys His Leu Gln Ala Val Val Leu His Leu Ala Arg Arg Ser Val
 65 70 75

tgt gtt cat ccc cag aac cgc agc ctg gct cgg tgg tta gaa cgc caa 289
 Cys Val His Pro Gln Asn Arg Ser Leu Ala Arg Trp Leu Glu Arg Gln
 80 85 90

ggg aaa agg ctc caa ggg act gta ccc agt tta aat ctg gta cta caa 337
 Gly Lys Arg Leu Gln Gly Thr Val Pro Ser Leu Asn Leu Val Leu Gln
 95 100 105

aag aaa atg tac tca aac ccc caa cag caa aac taa taaagcaaca 383
 Lys Lys Met Tyr Ser Asn Pro Gln Gln Gln Asn
 110 115 120

ttagacgaca 393

<210> 70
 <211> 912
 <212> DNA
 <213> Mus musculus

<220>
 <223> Mouse Lungkine cDNA

<220>
 <221> CDS

<222> (1) .. (504)

<300>

<308> AF082859/GenBank

<400> 70

atg gct gct caa ggc tgg tcc atg ctc ctg ctg gct gtc ctt aac cta 48
Met Ala Ala Gln Gly Trp Ser Met Leu Leu Leu Ala Val Leu Asn Leu
1 5 10 15

ggc atc ttc gtc cgt ccc tgt gac act caa gag cta cga tgt ctg tgt 96
Gly Ile Phe Val Arg Pro Cys Asp Thr Gln Glu Leu Arg Cys Leu Cys
20 25 30

att cag gaa cac tct gaa ttc att cct ctc aaa ctc att aaa aat ata 144
Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile Lys Asn Ile
35 40 45

atg gtg ata ttc gag acc att tac tgc aac aga aag gaa gtg ata gca 192
Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys Glu Val Ile Ala
50 55 60

gtc cca aaa aat ggg agt atg att tgt ttg gat cct gat gct cca tgg 240
Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp Pro Asp Ala Pro Trp
65 70 75 80

gtg aag gct act gtt ggc cca att act aac agg ttc cta cct gag gac 288
Val Lys Ala Thr Val Gly Pro Ile Thr Asn Arg Phe Leu Pro Glu Asp
85 90 95

ctc aaa caa aag gaa ttt cca ccg gca atg aag ctt ctg tat agt gtt 336
Leu Lys Gln Lys Glu Phe Pro Pro Ala Met Lys Leu Leu Tyr Ser Val
100 105 110

gag cat gaa aag cct cta tat ctt tca ttt ggg aga cct gag aac aag 384
Glu His Glu Lys Pro Leu Tyr Leu Ser Phe Gly Arg Pro Glu Asn Lys
115 120 125

aga ata ttt ccc ttt cca att cgg gag acc tct aga cac ttt gct gat 432
Arg Ile Phe Pro Phe Pro Ile Arg Glu Thr Ser Arg His Phe Ala Asp
130 135 140

tta gct cac aac agt gat agg aat ttt cta cgg gac tcc agt gaa gtc 480
Leu Ala His Asn Ser Asp Arg Asn Phe Leu Arg Asp Ser Ser Glu Val
145 150 155 160

agc ttg aca ggc agt gat gcc taa aagccactca tgaggcaaag agtttcaagg 534
Ser Leu Thr Gly Ser Asp Ala
165

aagctctcct cctggagttt tggcgttctc attcttatac tctattcccg cgtagtctg 594

gtgtatggat ctatgagctc tcttttaata ttttattata aatgttttat ttacttaact 654

tcctagtga a tgttcacagg tgactgctcc cccatcccca tttcttgata ttacatataa 714

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